<400> 19
taggctggca atttaactct gagacgtctt tcttgtatag agaataaaac atacgcgtgt   60

aaaagaaaac gcgtgaatcg aatgatgagt gttaacgttc gatcgagatg ccaccaaatc   120

ttttcattaa aatgaattgt ggaggacata ccacttttaa cgaggtcatt tccactgggt   180

gacatgtgga ctctactttg ggtggcatgt tcatatcttt ccacatcacc atgtaaacgt   240

gaaaacaccc accacactca cttacatctc aaacacatgt cttcattatc gtacgtagct   300

ccaaaaaaaa aaatgaaaac taggtttagt gattctattt cgcaatgtat aatatacaac   360

ttgtaaaaat aaaatatttg aataagcatt ataataaac ccaaagaggt gttagattta   420

tatacttaat tgtagctact aaatagagaa tcagagagaa tagtttttata tcttgcacga   480

aactgcatgc tttttgagac atg gca atc ttc cga agt aca cta gtt tta ctg   533
                         Met Ala Ile Phe Arg Ser Thr Leu Val Leu Leu
                         1   5   10

ctg atc ctc ttc tgc ctc acc act ttt gag gttcataact tttgtcttta   583
Leu Ile Leu Phe Cys Leu Thr Thr Phe Glu
            15   20

cttctccatg aatcatttgc ttcgtcttat ccttaattca tatgtgtttg atcaatgata   643

ataattcatc attctcttca g ctt cat gtt cat gct gct gaa gat tca caa   694

```
                    Leu His Val His Ala Ala Glu Asp Ser Gln
                             25                      30


gtc ggt gaa ggc gta gtg aaa att g gtatgtaacg ctaacatata          739
Val Gly Glu Gly Val Val Lys Ile
              35


tgtaaagtgt tatatctctg tttatatatg atttttaaac ggttaaaaac tagtcatatg     799


tgtataaata tatcatgtga ag at  tgc ggt ggg aga tgc aaa ggt aga tgc      850
                            Asp Cys Gly Gly Arg Cys Lys Gly Arg Cys
                                             45
```

Please insert a "40" under "Asp" above. Same type of error in Sequence
25, position 1452.

* *

Application No: 10521518   Version No: 2.0

Input Set:

Output Set:

Started:	2008-09-18 16:07:27.372
Finished:	2008-09-18 16:07:33.394
Elapsed:	0 hr(s) 0 min(s) 6 sec(s) 22 ms
Total Warnings:	0
Total Errors:	10
No. of SeqIDs Defined:	110
Actual SeqID Count:	110

Error code	Error Description
E 320	Wrong Nucleic Acid Designator, aa in SEQID (5)
E 320	Wrong Nucleic Acid Designator, at in SEQID (9)
E 320	Wrong Nucleic Acid Designator, aa in SEQID (11)
E 320	Wrong Nucleic Acid Designator, aa in SEQID (13)
E 320	Wrong Nucleic Acid Designator, ag in SEQID (17)
E 323	Invalid/missing amino acid numbering SEQID (19) POS (800)
E 320	Wrong Nucleic Acid Designator, at in SEQID (19)
E 323	Invalid/missing amino acid numbering SEQID (25) POS (1452)
E 320	Wrong Nucleic Acid Designator, at in SEQID (25)
E 320	Wrong Nucleic Acid Designator, ca in SEQID (27)

Met Ala Ala Glu Gln Pro Leu Asn Gly Ala Phe Tyr Gly Pro Ser Val
1   5   10   15

Pro Pro Pro Ala Pro Lys Gly Tyr Tyr Arg Arg Gly His Gly Arg Gly
            20   25   30

Cys Gly Cys Cys Leu Leu Ser Leu Phe Val Lys Val Ile Ile Ser Leu
        35   40   45

Ile Val Ile Leu Gly Val Ala Ala Leu Ile Phe Trp Leu Ile Val Arg
    50   55   60

Pro Arg Ala Ile Lys Phe His Val Thr Asp Ala Ser Leu Thr Arg Phe
65   70   75   80

Asp His Thr Ser Pro Asp Asn Ile Leu Arg Tyr Asn Leu Ala Leu Thr
                85   90   95

Val Pro Val Arg Asn Pro Asn Lys Arg Ile Gly Leu Tyr Tyr Asp Arg
                100   105   110

Ile Glu Ala His Ala Tyr Tyr Glu Gly Lys Arg Phe Ser Thr Ile Thr
        115   120   125

Leu Thr Pro Phe Tyr Gln Gly His Lys Asn Thr Thr Val Leu Thr Pro
    130   135   140

Thr Phe Gln Gly Gln Asn Leu Val Ile Phe Asn Ala Gly Gln Ser Arg
145   150   155   160

Thr Leu Asn Ala Glu Arg Ile Ser Gly Val Tyr Asn Ile Glu Ile Lys
                165   170   175

Phe Arg Leu Arg Val Arg Phe Lys Leu Gly Asp Leu Lys Phe Arg Arg
                180   185   190

Ile Lys Pro Lys Val Asp Cys Asp Asp Leu Arg Leu Pro Leu Ser Thr
        195   200   205

Ser Asn Gly Thr Thr Thr Thr Ser Thr Val Phe Pro Ile Lys Cys Asp
    210   215   220

Phe Asp Phe
225

<210>   2
<211>   416
<212>   PRT
<213>   Arabidopsis thaliana

<400>   2

Met Val Arg Ser Asn Asp Val Lys Phe Gln Val Tyr Asp Ala Glu Leu
1   5   10   15

Thr His Phe Asp Leu Glu Ser Asn Asn Asn Leu Gln Tyr Ser Leu Ser
            20   25   30

Leu Asn Leu Ser Ile Arg Asn Ser Lys Ser Ser Ile Gly Ile His Tyr
        35   40   45

Asp Arg Phe Glu Ala Thr Val Tyr Tyr Met Asn Gln Arg Leu Gly Ala
    50   55   60

Val Pro Met Pro Leu Phe Tyr Leu Gly Ser Lys Asn Thr Met Leu Leu
65   70   75   80

Arg Ala Leu Phe Glu Gly Gln Thr Leu Val Leu Leu Lys Gly Asn Glu
                85   90   95

Arg Lys Lys Phe Glu Asp Asp Gln Lys Thr Gly Val Tyr Arg Ile Asp
                100   105   110

Val Lys Leu Ser Ile Asn Phe Arg Val Met Val Leu His Leu Val Thr
        115   120   125

Trp Pro Met Lys Pro Val Val Arg Cys His Leu Lys Ile Pro Leu Ala
        130   135   140

Leu Gly Ser Ser Asn Ser Thr Gly Gly His Lys Lys Met Leu Leu Ile
145   150   155   160

Gly Gln Leu Val Lys Asp Thr Ser Ala Asn Leu Arg Glu Ala Ser Glu
                165   170   175

Thr Asp His Arg Arg Asp Val Ala Gln Ser Lys Lys Ile Ala Asp Ala
        180   185   190

Lys Leu Ala Lys Asp Phe Glu Ala Ala Leu Lys Glu Phe Gln Lys Ala
        195   200   205

Gln His Ile Thr Val Glu Arg Glu Thr Ser Tyr Ile Pro Phe Asp Pro
        210   215   220

Lys Gly Ser Phe Ser Ser Ser Glu Val Asp Ile Gly Tyr Asp Arg Ser
225   230   235   240

Gln Glu Gln Arg Val Leu Met Glu Ser Arg Arg Gln Glu Ile Val Leu
                245   250   255

Leu Asp Asn Glu Ile Ser Leu Asn Glu Ala Arg Ile Glu Ala Arg Glu
                260   265   270

Gln Gly Ile Gln Glu Val Lys His Gln Ile Ser Glu Val Met Glu Met
        275   280   285

Phe Lys Asp Leu Ala Val Met Val Asp His Gln Gly Thr Ile Asp Asp
        290   295   300

Ile Asp Glu Lys Ile Asp Asn Leu Arg Ser Ala Ala Ala Gln Gly Lys
305   310   315   320

Ser His Leu Val Lys Ala Ser Asn Thr Gln Gly Ser Asn Ser Ser Leu
                325   330   335

Leu Phe Ser Cys Ser Leu Leu Leu Phe Phe Phe Leu Ser Gly Asp Leu
            340   345   350

Cys Arg Cys Val Cys Val Gly Ser Glu Asn Pro Arg Leu Asn Pro Thr
        355   360   365

Arg Arg Lys Ala Trp Cys Glu Glu Glu Asp Glu Glu Gln Arg Lys Lys
    370   375   380

Gln Gln Lys Lys Lys Thr Met Ser Glu Lys Arg Arg Arg Glu Glu Lys
385   390   395   400

Lys Val Asn Lys Pro Asn Gly Phe Val Phe Cys Val Leu Gly His Lys
                405   410   415

<210>   3
<211>   1634
<212>   DNA
<213>   Arabidopsis thaliana

<220>
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<222>   (501)..(563)
<223>   signal sequence (exon 1)

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<222>   (655)..(708)
<223>   propeptide (exon 2)

<220>
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<222>   (797)..(856)
<223>   propeptide (exon 3)

<220>
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<222>   (955)..(1131)
<223>   conserved cysteine motif (exon 4)

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ctatctctct cagtgtcaca atgtctgaac taagagacag ctgtaaacta tcattaagac      120

ataaactacc aaagtatcaa gctaatgtaa aaattactct catttccacg taacaaattg      180

agttagctta agatattagt gaaactaggt ttgaattttc ttcttcttct tccatgcatc      240

ctccgaaaaa agggaaccaa tcaaaactgt ttgcatatca aactccaaca ctttacagca      300

aatgcaatct ataatctgtg atttatccaa taaaaacctg tgatttatgt ttggctccag      360

cgatgaaagt ctatgcatgt gatctctatc caacatgagt aattgttcag aaaataaaaa      420

gtagctgaaa tgtatctata taagaatca tccacaagta ctattttcac acactacttc       480

aaaatcacta ctcaagaaat atg aag aag atg aat gtg gtg gct ttt gtt acg      533
                        Met Lys Lys Met Asn Val Val Ala Phe Val Thr
                         1           5                       10

ctg atc atc tct ttt ctt ctg ctt tct cag gtaaactgtt aaaaccattt          583
Leu Ile Ile Ser Phe Leu Leu Leu Ser Gln
            15                  20

tcaagactac cttttctcta tttcagacaa accaaagtaa aacaatgaaa aatctctctg       643

gtctttcata g gta ctt gca gag ttg tca tca tcc agc aac aat gaa act       693
             Val Leu Ala Glu Leu Ser Ser Ser Ser Asn Asn Glu Thr
                  25                      30

tcc tct gtt tct cag gtaagagtga tacaaaaaca tactaaacaa actttcaaga        748
Ser Ser Val Ser Gln
35

gagtaatata taaggaaatg ttggcttctt ttttttgttg ctaatcag acg aat gac       805
                                                        Thr Asn Asp
                                                         40

gag aac caa act gcg gcg ttt aag aga aca tac cac cat cgt cca aga        853
Glu Asn Gln Thr Ala Ala Phe Lys Arg Thr Tyr His His Arg Pro Arg
         45                  50                  55

atc agttagtcta ctctttcaac actctaattc ctttgttcta agtatttttt           906
Ile

ttgcccccca caaccttttt tttattaaat gagccaattt ttatagat tgt ggg cat      963
                                                        Cys Gly His
                                                         60

gca tgc gca agg aga tgc agt aag aca tcg agg aag aaa gtt tgt cac       1011
Ala Cys Ala Arg Arg Cys Ser Lys Thr Ser Arg Lys Lys Val Cys His
         65                  70                  75

aga gcc tgt gga agt tgt tgt gcc aag tgt cag tgt gtg ccg ccg gga       1059
Arg Ala Cys Gly Ser Cys Cys Ala Lys Cys Gln Cys Val Pro Pro Gly
   80                  85                  90
```

```
acc tcc ggc aac aca gca tca tgt cct tgc tac gcc agt atc cgt aca        1107
Thr Ser Gly Asn Thr Ala Ser Cys Pro Cys Tyr Ala Ser Ile Arg Thr
95                  100             105                 110

cat ggc aat aaa ctc aaa tgt cct taaaagactt ctcatttctc aactatagtc       1161
His Gly Asn Lys Leu Lys Cys Pro
                115

tcatcttctg attatgtttc ttcttttgtt atgttgcatg tgtgatgtgt gagcttatta      1221

ttatgttgat tgttgacata attcaactat ataatttgta tcgattccga ataataagat      1281

gagtgatttt attggctatt aagttttttt tttttttttt tgggcacaat ggctattaag      1341

ttttaaacat ctgattttat tggttacaaa aaacaacaaa gtttcatttt catattaaca      1401

caaaatctcc atacatatta ccaaaccaaa aaaatacaca agggggagag agaccaacgg      1461

ttcttggttc agagtttgca tcttgtttga gccgtcaccg tttcttagac ttaacagcca      1521

caacaccttt ataaagcttc acgcgatcct tcaacgcatc tcgccgaggc cgagccacct      1581

tattgtttgg atcaaacaac aaaacttctt caaacgcatt caatgccaaa ggc            1634



<210>   4
<211>   118
<212>   PRT
<213>   Arabidopsis thaliana

<400>   4

Met Lys Lys Met Asn Val Val Ala Phe Val Thr Leu Ile Ile Ser Phe
1               5                   10                  15


Leu Leu Leu Ser Gln Val Leu Ala Glu Leu Ser Ser Ser Ser Asn Asn
            20                  25                  30


Glu Thr Ser Ser Val Ser Gln Thr Asn Asp Glu Asn Gln Thr Ala Ala
        35                  40                  45


Phe Lys Arg Thr Tyr His His Arg Pro Arg Ile Cys Gly His Ala Cys
    50                  55                  60


Ala Arg Arg Cys Ser Lys Thr Ser Arg Lys Lys Val Cys His Arg Ala
65                  70                  75                  80


Cys Gly Ser Cys Cys Ala Lys Cys Gln Cys Val Pro Pro Gly Thr Ser
                85                  90                  95


Gly Asn Thr Ala Ser Cys Pro Cys Tyr Ala Ser Ile Arg Thr His Gly
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Asn Lys Leu Lys Cys Pro
        115

<210>   5
<211>   1453
<212>   DNA
<213>   Arabidopsis thaliana

<220>
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<222>   (501)..(533)
<223>   signal peptide (exon 1)

<220>
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<222>   (664)..(691)
<223>   propeptide (exon 2)

<220>
<221>   CDS
<222>   (772)..(950)
<223>   conserved cysteine motif (exon 3)

<400>   5
gaaaaaaaga agaaaagata atggtccgta ttaatatagt tgaaaacttg aaactacttt   60

ttagtttgta tataatacag tagactaggg atccagttga gtttctttct ttattttgag   120

tttgtgttta tgtttgattt tacgtttttta tatgtaaata agatattttta cgaattatgg   180

ttttatttgg gtagaagttg tagaatgact taaacaatca agtggcagaa tgagatatat   240

aaagtaatat aatatatgta ccgttattaa cttattgtac atgtgaatga ggaagcttac   300

acacacacac cttctataaa tagctgacaa aactggttgt tacacacaac acattcataa   360

atctctcaaa gtaagaacta agagctttac tacagtccta ctctctacac atcttctctc   420

tctctcaaga gctagtcatg gccaaactca taacttcttt tctcttactc acaattttat   480

tcactttcgt ttgtctcact atg tca aaa gaa gct gag tac cat cca gaa agt   533
                       Met Ser Lys Glu Ala Glu Tyr His Pro Glu Ser
                        1   5   10

gtaagttttt attttttggt aaaatagaaa gtgtaagttt tataattcat tcaattgttt   593

ttgcctttcc ctttctattt attgctataa atctaatacc cgcgttaaaa tttgttttga   653

aattaaacag tat gga cca gga agt ctg aaa tca tac c gtaagtaaaa   701
           Tyr Gly Pro Gly Ser Leu Lys Ser Tyr
                     15   20

```
acttcttctt cttttatgaa tcttgtttct tattatatat caaataaaaa ctcgattatc      761

atgattgcag aa  tgt gga gga caa tgc aca agg aga tgt agc aac aca         809
              Gln Cys Gly Gly Gln Cys Thr Arg Arg Cys Ser Asn Thr
                      25                  30

aag tat cat aag cca tgc atg ttc ttc tgc caa aag tgt tgt gct aaa        857
Lys Tyr His Lys Pro Cys Met Phe Phe Cys Gln Lys Cys Cys Ala Lys
    35                  40                  45

tgc ctt tgt gtc cct cca ggc acg tac ggc aac aaa caa gtg tgt cct        905
Cys Leu Cys Val Pro Pro Gly Thr Tyr Gly Asn Lys Gln Val Cys Pro
50                  55                  60                  65

tgt tac aac aac tgg aag act caa caa ggt gga cca aaa tgt cca            950
Cys Tyr Asn Asn Trp Lys Thr Gln Gln Gly Gly Pro Lys Cys Pro
                70                  75                  80

taaacaaaaa cattgagaga gaaaccccaa tctgtttcct attttattta attatttcca     1010

gtatgctttt gttgtcgtga tggttaaatt atagtgtttt tgcaggtatc atttatcatc     1070

gataaacaat atcatataaa atcttctatg tttctttcac gttttgtttc ttttgttgta     1130

gtcaatacac gaaatgtgta tggaccttct aattaggaat atataaaatt ttatttatta     1190

attagataat ctttcgtata gttaaaattc caaggattac ttttgattcg tttgggacaa     1250

tctattttat attttacttt ctaagtttgt ataactatat cttaaaagtg ttagacagag     1310

tcctaatgat tttagtataa ttgttactat ttagttacgc ttcgaaaatt tggaactttt     1370

ccaaagtggt ctatatcaat ttgattcact aatctgcgct tccttctagt tttttacaat     1430

tatggagatt tttcgacgat gat                                            1453



<210>   6
<211>   80
<212>   PRT
<213>   Arabidopsis thaliana

<400>   6

Met Ser Lys Glu Ala Glu Tyr His Pro Glu Ser Tyr Gly Pro Gly Ser
1               5                   10                  15


Leu Lys Ser Tyr Gln Cys Gly Gly Gln Cys Thr Arg Arg Cys Ser Asn
            20                  25                  30


Thr Lys Tyr His Lys Pro Cys Met Phe Phe Cys Gln Lys Cys Cys Ala
        35                  40                  45


Lys Cys Leu Cys Val Pro Pro Gly Thr Tyr Gly Asn Lys Gln Val Cys
```

```
                50                      55                      60


Pro Cys Tyr Asn Asn Trp Lys Thr Gln Gln Gly Gly Pro Lys Cys Pro
65                      70                      75                      80



<210>   7
<211>   1472
<212>   DNA
<213>   Arabidopsis thaliana



<220>
<221>   CDS
<222>   (501)..(566)
<223>   signal sequence (exon 1)


<220>
<221>   CDS
<222>   (669)..(708)
<223>   propeptide (exon 2)


<220>
<221>   CDS
<222>   (791)..(969)
<223>   conserved cysteine motif (exon 3)


<400>   7
cacaactttt atacgcacca ccaaccgacc cattttgaaa aagagaaaat aaaccacaaa      60

aacacacata aataatatgc tgataacaat gtcttaaaaa tctatttacc atttctagta     120

atcaatatct attgcaaaaa atatttataa gaatacaaat gaaaatgat aaaatacaaa      180

tgatttctca attacctaaa aaatataaaa atgtcttact ttattttcag ccactgttgg     240

aaagtacttg caatcatatc gtattttgaa ttataaaact cagaaacaat tattttccct     300

gaaaagttaa aactttaat aagatattta taaaataaaa agaatagtct agaccgaaaa      360

tggggtcggt tgtccatcca aaggagtgct ataaatagaa ccctccaagt tctcattagg     420

acacaacaac taaaaccaca tttatcatta cagtctgatt tgagctaagt tctctcatca     480

taaactctcc ttggagaatc atg gct att tca aaa gct ctt atc gct tct ctt     533
                         Met Ala Ile Ser Lys Ala Leu Ile Ala Ser Leu
                         1               5                       10

ctc ata tct ctt ctt gtt ctc caa ctc gtc cag gctgatgtcg tacgtctttt    586
Leu Ile Ser Leu Leu Val Leu Gln Leu Val Gln
            15                  20

tcatcacaaa ctaattatac tcaatataat acttatgttt tcaaaaacat atttctcaca    646

tgttacaaca atattcttgc ag gaa aac tca cag aag aaa aat ggt tac gca     698
                         Glu Asn Ser Gln Lys Lys Asn Gly Tyr Ala
```

```
aag aag atc g gtaattatat gatttttatt aaacctaacg ttaaatttag          748
Lys Lys Ile
        35


agtgagatta ataatctgtg tttttctttc ttgtatatat ag at   tgt ggg agt     801
                                                    Asp Cys Gly Ser



gcg tgt gta gca cgg tgc agg ctt tcg agg agg ccg agg ctg tgt cac    849
Ala Cys Val Ala Arg Cys Arg Leu Ser Arg Arg Pro Arg Leu Cys His
40                  45                  50                  55

aga gcg tgc ggg act tgc tgc tac agg tgc aac tgt gtg cct ccg ggt    897
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